FIGURE 1

P2P cDNA
(5173 base pairs)

5' |████████████████████████████████| 3'
1 └─139   Open Reading Frame   4353┘   5173
              (4214 base pairs)

P2P cDNA Deduced Protein
(1404 amino acids)

1   1404

                                    C130
                                  (853-1404)

GST P2P   Fusion
(1-332)   GST P2P   Proteins
              (484-688)   GST P2P
                         (753-908) GST P2P
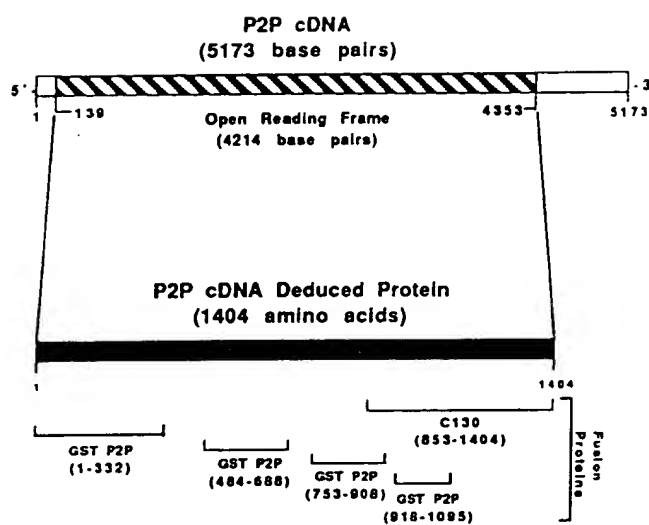   (918-1095)

FIGURE 2

```
MMEVKDPNMKGAMLTNTGKYAIPTIDAEAYAIGKKEKPPFLPEEPSSSSEEDDPIPAELL      60
CLICKDIMTDAVVIPCCGNSSCDECIRTTLLESDKHTCPTC HQNDVSPDALIANKFLRQA    120
VNNFKNETGYTKRLRKQLPPFLFLVPPPRPLSQRNLQPRSRSPILRQQDPVVFRYTVSPT    180
CSDTKTAGSCSDSGTLSRLPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDITATVSISV    240
HSEKSDGPFRDSDNKLLPAAALTSEHSKGASSIAITALMEEKGVPGTSPWNSIFVGQSLL    300
HGQLIPTTGPVRINAARPGGGRPGWEHSNKLGYLVSPPQQIRRGERSCYRSINRGRHHSE    360
RSQRTQSPSLPATPCFVPVPPPPLYPPPPHTLPLPPGVPPPQFSPQFPSSQPPTAGYSVP    420
PPGFPPAPANISTACFSPGVPTAHSNTMPTTQAPLLSREEFYREQNDKGRESKFPYSGSS    480
YSRSSYTDSSQGLAQHIHALTLSPSAAHTLDLLHDHPHPPEEAEARSAMIVHMPDLMDIA    540
HARSRSPPYRRYRSRSRSPPEFRGQSPTKRNVPREEKEREYFNRYREVPPPYDIKAYYGR    600
SVDFRDPFEKERYREWERKYREWYEKYYKGYAVGAQPRPSANREDFSPERLLPLNIRNSP    660
FTRGRREDYAAGQSHRNRNLGGNYPEKLSTRDSHNAKDNPKSKEKESENVPGDGKGNKHK    720
KHRKRRNEEKGEESESFLNPELLETSRKCRGSSGIDETKTDTLFVLPSRDDATPVRDEPM    780
DAESITFKSVSDKDKREKDKPKVKSDKTKRKSDGSATAKKDNVLKPSKGPQEKVDGDREK    840
SPRSEPPLKKAKEEATKIDSVKPSSSSQKDEKVTGTPRKAHSKSAKDTRRQSQPRTRRSK    900
RTVPKTSSQKSQPVRTRRPRSLRKINYLIAREKNEREKRKKSVDKDFESSSMKISKVEGT    960
EIVKPSPKRKMEGDVEKLERTPEKDKIASSTTPAKKIKLNRETGKKIGNAENASTTKEPS   1020
EKLESTSSKIKQEKVKGKAKRKVAGSEGSSSTLVDYTSTSSTGGSPVRKSEEKTDTKRTV   1080
IKTMEEYNNDNTAPAEDVIIMIQVPQSKWDKDDFESEEEDVKTTQPIQSVGKPSSIIKNV   1140
TTKPSATAKYTEKESEQPEKLQKLPKEASHELMQHELRSSKGSASSEKGRAKDREHSGSE   1200
KDNPDKRKSGAQPDKESTVDRLSEQGHFKTLSQSSKETRTSEKHESVRGSSNKDFTPGRD   1260
KKVDYDSRDYSSSKRRDERGELARRKDSPPRGKESLSGQKSKLREERDLPKKGAESKKSN   1320
SSPPRDKKPHDHKAPYETKRPCEETKPVDKNSGKEREKHAAEARNGKESSGANCHVYLTR   1380
QTLPWRRSWLLGRWRRAPSSRNPS                                      1404
```

FIGURE 3

A.

B.

FIGURE 4

GST

GST-P2P(1-332)

GST-P2P(494-688)

GST-P2P(918-1095)

GST-P2P(753-909)

Normal Rabbit Sera

Anti-RB(IF-8)

Crude Lysate

RB

GST-P2P
(753-909)

GST

E1a   E1a
 -      +

RB —

Fig. 5

                                                            60
                                                             *
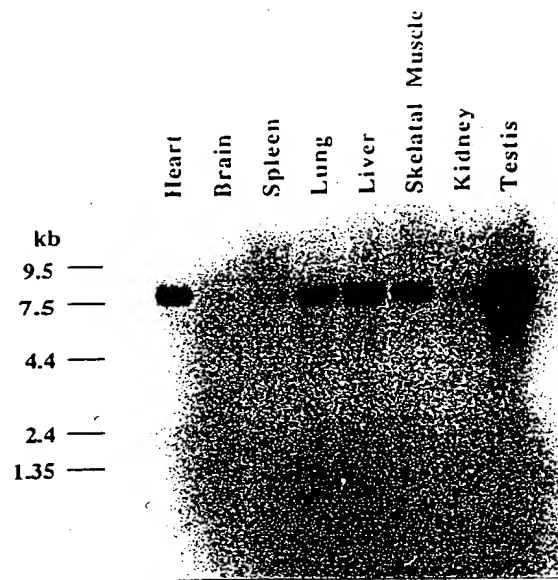
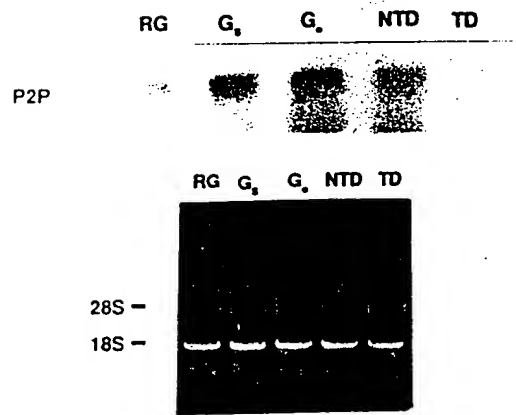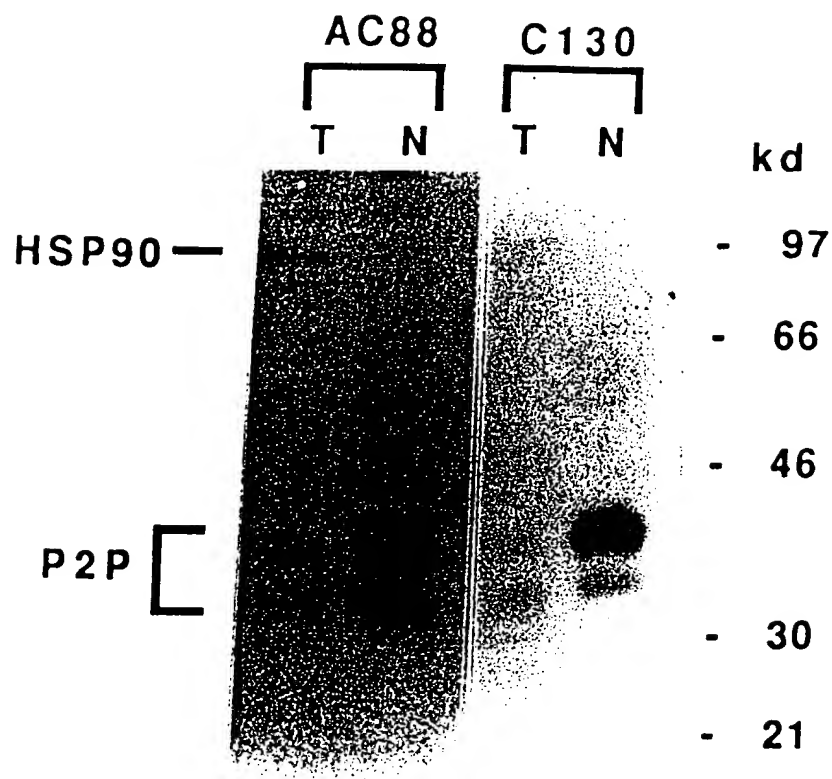AGGTCCACCACCTCCATCTTACACCTGCTTTCGTTGTGGTAAACCTGGTCATTATATTAAGAAT
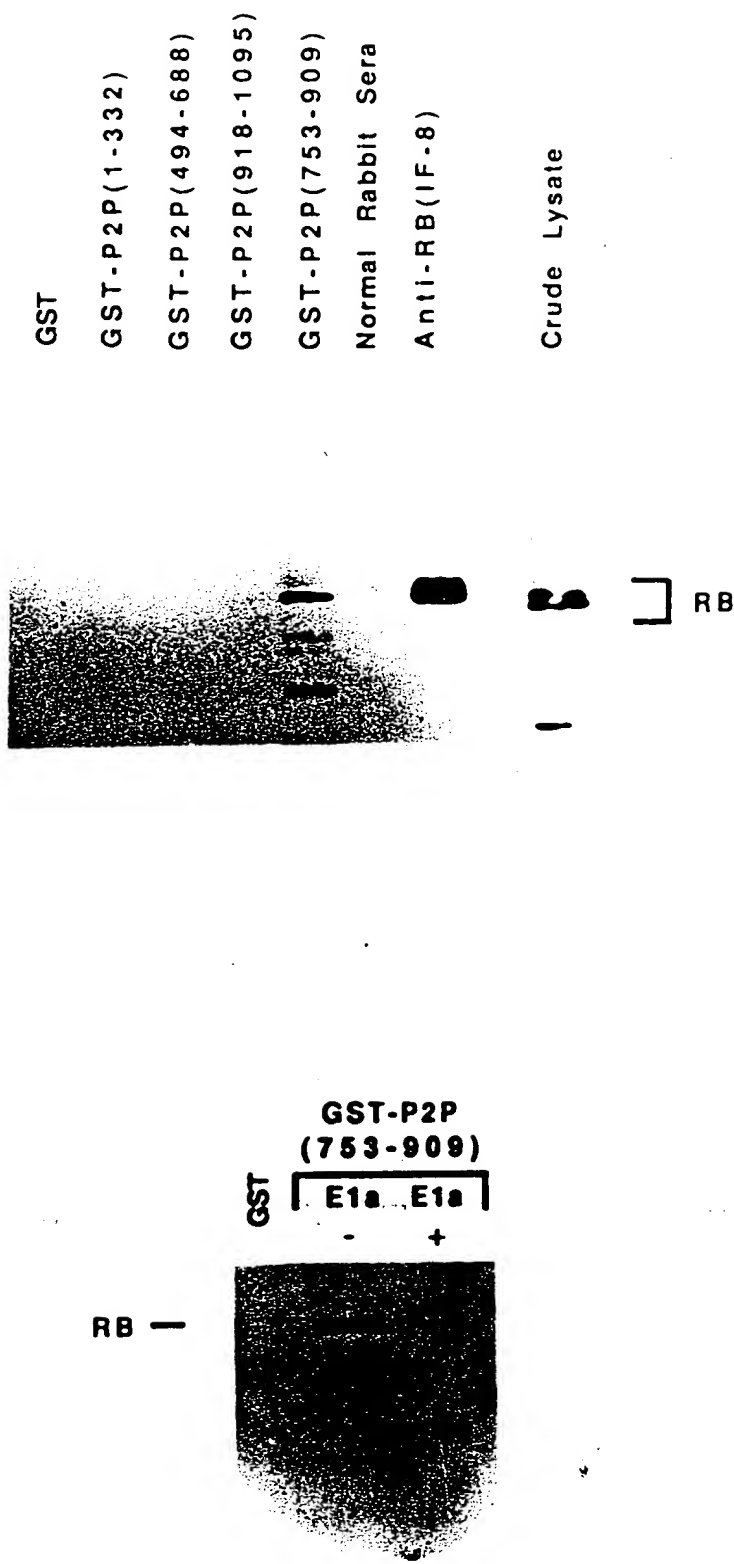   120
                                                             *

TGCCAACAAATGGGGATAAGAACTTTGAATCTGGTCCTAGGATCAAAAAGAGCACTGGAATTCC
                                                    180
                                                       *

TAGAAGTTTTATGATGGAAGTGAAAGATCCTAACATGAAAGGTGCAATGCTTACCAACACTGGA
                                                240
                                                   *

AAATATGCAATACCAACTATAGATGCAGAGGCCTATGCAATCGGGAAGAAAGAGAAACCACCCT
                                            300
                                               *

TCTTACCAGAGGAGCCATCATCATCTTCAGAAGAAGATGATCCTATCCCAGCAGAGCTCTTGTG
                                        360
                                           *

CCTCATCTGCAAAGACATCATGACTGATGCTGTGGTCATTCCCTGCTGTGGAAACAGTTCATGT
                                    420
                                       *

GATGAATGTATAAGAACGACACTCTTGGAGTCAGATAAACATACATGTCCAACATGTCACCAAA
                            480
                               *

ATGATGTTTCTCCTGATGCTTTAATTGCCAACAAGTTTTTACGACAGGCTGTTAATAACTTTAA
                        540
                           *

AAATGAAACTGGCTATACAAAACGACTACGAAAACAGTTACCTCCATTTTTATTTTTAGTACCA
                    600
                       *

CCACCAAGACCACTCAGTCAGCGGAACCTACAGCCTCGTAGTAGATCTCCAATACTAAGACAGC
                660
                   *

AGGATCCTGTAGTATTCAGGTACACTGTCTCGCCTACCTGCTCCGATACTAAGACAGCAGGATC
            720
               *

CTGTAGTGATTCAGGTACACTGTCTCGCCTACCTGCTCCGTCTATATCTTCATTAACTTCTAAT
            780
               *

CAGTCTTCCTTGGCCCCTCCTGTGTCTGGAAATCCGTCTTCTGCTCCAGCTCCAGTACCTGATA
        840
           *

TAACTGCAACCGTGTCTATATCAGTCCACTCAGAAAAATCGGATGGACCTTTTCGGGATTCTGA
900   960
   *   *

TAATAAATTATTGCCAGCTGCCGCCCTTACATCAGAACATTCAAAGGGAGCCTCTTCAATTGCT
                                                    1020
                                                       *

ATTACTGCTCTTATGGAAGAAAAAGGGGTACCAGGTACCAGTCCTTGGAACTCCATCTTTGTTG

Fig. 6A

```
                                                                  1080
                                                                   *
        GACAGTCATTATTACATGGACAGTTGATTCCCACAACTGGCCCAGTAAGAATCAATGCTGCTCG ,
                                                           1140
                                                            *
        TCCAGGTGGTGGCCGGCCAGGCTGGGAGCATTCCAACAAGCTTGGGTACCTAGTTTCTCCACCA
                                                    1200
                                                     *
        CAGCAAATTAGAAGAGGAGAAAGAAGCTGTTACAGAAGTATAAACCGCGGGCGACACCACAGCG
                                               1260
                                                *
        AACGATCACAGAGGACTCAAAGCCCATCACTTCCAGCAACTCCATGCTTTGTGCCCGTTCCACC
                                          1320
                                           *
        ACCTCCTTTGTATCCGCCTCCTCCCCATACACTTCCTCTTCCTCCAGGTGTACCTCCTCCACAG
                                     1380
                                      *
        TTTTCTCCTCAGTTTCCCTCCTCCCAGCCTCCAACAGCAGGATATAGTGTCCCTCCTCCAGGAT
                               1440
                                *
        TTCCACCAGCTCCTGCCAATATATCAACAGCTTGCTTTTCACCAGGTGTTCCCACTGCCCATTC
                          1500
                           *
        AAATACCATGCCCACAACACAAGCACCTCTTTTGTCCAGGGAAGAATTCTATAGAGAGCAAAAC
                    1560
                     *
        GACAAAGGAAGAGAGTCTAAATTTCCCTATAGTGGGTCATCGTATTCAAGAAGTTCATACACTG
              1620
               *
        ACTCAAGTCAAGGTCTGGCTCAACACATTCACGCTCTTACTCTCAGTCCTTCAGCTGCTCACAC
            1680
             *
        TCTCGATCTTCTTCACGATCATCCCCATCCTCCAGAAGAGGCAGAGGCAAGATCTGCAATGATT
            1740
             *
        GTTCACATGCCAGATCTCATGGATATCGCCCATGCTAGGTCAAGGTCACCTCCCTATAGACGAT
           1800
            *
        ATCGCTCACGGTCCAGATCTCCTCCAGAATTTAGGGGACAGTCTCCCACTAAACGTAATGTACC
        1860                                                      1920
         *                                                         *
        TCGAGAAGAGAAAGAACGTGAGTATTTTAATAGATACAGAGAAGTTCCACCCCCTTATGACATC
                                                           1980
                                                            *
        AAAGCCTATTATGGGCGGAGTGTCGACTTTAGAGACCCATTTGAGAAAGAACGCTACCGGGAAT
                                                     2040
                                                      *
        GGGAAAGGAAATACCGAGAGTGGTATGAGAAGTACTACAAAGGGTACGCGGTGGGAGCTCAACC
```

Fig. 6B

                                                    2100
                                                     *
TAGACCCTCAGCCAATAGAGAGGACTTTTCTCCAGAGAGACTCTTACCTCTTAATATCAGAAAT
                                        2160
                                         *
TCACCCTTCACAAGAGGCCGCAGAGAAGACTATGCTGCTGGACAAAGTCATAGAAATAGAAATC
                              2220
                               *
TAGGTGGCAACTATCCAGAAAAGCTTTCAACAAGGGACAGTCACAATGCAAAAGATAATCCAAA
                        2280
                         *
ATCGAAGGAGAAGGAGAGTGAGAATGTTCCAGGAGACGGCAAAGGGAACAAGCATAAGAAACAC
                     2340
                      *
AGGAAACGAAGAAACGAAGAAAAGGGGGAAGAGAGTGAGAGCTTCCTGAACCCAGAGCTACTGG
                  2400
                   *
AGACGTCTAGGAAATGCAGGGGATCGTCAGGGATTGATGAAACGAAGACAGATACACTGTTTGT
                 2460
                  *
TCTCCCAAGCAGAGACGATGCTACACCTGTTAGGGATGAGCCAATGGACGCAGAATCGATCACT
              2520
               *
TTCAAGTCAGTATCTGACAAAGACAAGAGGGAAAAGGATAAGCCAAAAGTAAAAAGTGACAAGA
             2580
              *
CCAAACGGAAAAGTGACGGGTCTGCTACAGCCAAGAAAGACAATGTTTTAAAACCTTCTAAAGG
          2640
           *
ACCTCAAGAAAAGGTAGATGGAGACCGTGAAAAGTCTCCTCGGTCTGAGCCGCCACTCAAAAAA
        2700
         *
GCCAAAGAGGAGGCTACAAAGATTGACTCTGTAAAACCTTCCTCGTCTTCTCAGAAGGATGAGA
      2760
       *
AGGTCACTGGAACCCCTAGAAAAGCCCATTCTAAATCTGCAAAAGACACCAGGAGGCAAAGCCA
2820   2880
 *   *
GCCAAGGACGAGAAGGTCAAAAAGGACTGTTCCAAAGACATCAAGTCAGAAAAGCCAGCCAGTA
                                               2940
                                                *
AGGACGAGAAGGCCAAGAAGCCTGAGAAAAATAAACTACTTGATAGCAAGGGAGAAAAACGAAA
                                       3000
                                        *
GAGAAAAACGGAAGAAGAGTGTAGATAAAGATTTTGAGTCGTCTTCAATGAAAATCTCTAAAGT

Fig. 6C

```
                                              3060
                                               *
AGAAGGAACAGAAATAGTGAAACCATCACCAAAACGGAAAATGGAAGGTGATGTTGAAAAGCTG
                                              3120
                                               *
GAAAGGACCCCAGAAAAGGACAAGATTGCATCATCAACTACTCCAGCCAAAAAAATCAAACTCA
                                              3180
                                               *
ACAGAGAAACTGGAAAAAAAATTGGAAATGCAGAAAATGCATCTACTACAAAAGAACCCTCTGA
                                       3240
                                        *
AAAATTGGAGTCAACATCTAGCAAAATCAAACAGGAAAAAGTCAAGGGAAAGGCCAAACGGAAA
                                 3300
                                  *
GTAGCTGGGTCGGAAGGCTCCAGCTCCACGCTTGTGGATTACACCAGTACAAGTTCAACTGGAG
                             3360
                              *
GCAGTCCTGTGAGGAAATCTGAAGAAAGACAGATACAAAGCGAACAGTCATTAAAACTATGGA
                          3420
                           *
GGAATATAATAATGATAACACAGCTCCTGCTGAAGATGTTATAATTATGATCCAGGTTCCTCAG
                       3480
                        *
TCCAAATGGGATAAAGATGACTTTGAGTCTGAAGAAGAAGATGTTAAAACCACACAACCTATAC
                  3540
                   *
AGAGTGTAGGGAAACCATCGAGTATTATAAAAAATGTCACTACTAAGCCATCGGCTACGGCTAA
              3600
               *
GTACACCGAGAAGGAAAGCGAGCAGCCCGAGAAACTGCAGAAGCTTCCCAAGGAGGCGAGCCAC
           3660
            *
GAGCTGATGCAGCACGAGCTCAGGAGCTCAAAGGGCAGTGCGTCCAGTGAGAAGGGCAGAGCCA
        3720
         *
AGGACCGGGAGCACTCAGGGTCGGAGAAGGACAACCCTGACAAGAGGAAGAGCGGTGCCCAGCC
3780                                                            3840
  *                                                              *
AGACAAGGAGAGCACTGTGGACCGCCTGAGTGAGCAGGGACATTTTAAGACTCTCTCTCAGTCT
                                                    3900
                                                     *
TCCAAAGAGACCAGGACTTCAGAGAAGCACGAGTCTGTTCGTGGTTCCTCAAATAAAGACTTCA
                                               3960
                                                *
CTCCTGGTAGAGACAAGAAAGTGGACTACGACAGCAGGGATTATTCCAGTTCCAAGCGAAGAGA
                                            4020
                                             *
CGAGAGAGGTGAATTAGCAAGGAGAAAAGACTCTCCTCCCCGGGGCAAAGAGTCTCTGTCTGGG
```

Fig. 6D

4080
*

CAGAAAAGCAAGCTGAGGGAGGAGAGAGATTTACCTAAAAAGGGGGCCGAGTCAAAAAAAGTA

4140
*

ATTCTAGCCCCCCAAGAGACAAAAAGCCTCATGATCATAAAGCCCCCTACGAAACTAAACGCCC

4200
*

ATGTGAAGAGACAAAGCCTGTAGATAAAAACTCTGGGAAGGAGCGGGAGAAGCATGCTGCTGAA

4260
*

GCTCGCAATGGGAAAGAGTCCAGTGGTGCAAACTGCCATGTATACCTAACCCGCCAGACCCTCC

4320
*

CATGGAGAAGGAGCTGGCTGCTGGGCAGGTGGAGAAGAGCGCCGTCAAGCCGAAACCCCAGCTG

4380
*

AGCCATTCCTCGAGGCTTTCCTCTGACCTGACCCGGGAGACGAACGAGGCAGCCTTTGAACCAG

4440
*

ATTATAATGAGAGCGACAGTGAGAGTAATGTGTCTGTGAAGGAAGAAGAAGCTGTTGCCAGTAT

4500
*

CTCCAAGGACTTGAAAGAGAAAACAACAGAGAAAGCGAAAGAGAGCTTGACTGTAGCAACGGCC

4560
*

AGCCAGCCAGGTGCAGACAGGAGCCAGAGCCAAAGTAGCCCAGTGTTAGTCAGTAGAGTCATAG

4620
*

CCTTCGGAGCCAGACCCGAAGCCACAGCAGCAGTGCCAGCTCAGCCGGAAGGCCAGGACAGCAA

4680
*

AAAGAAGAAGAAGAAGAAGGAGAAGAAAAACGACAAGAAGCATAAAAAGCACAAGAAGCACAAG

4740   4800
*   *

AAGCACGCAGGCCGACGGCGACGTGGAGAAGAGCCAGAAACACAAACACAAGAAGAAGAAGGCC

4860
*

AAGAAGAACAAAGACAAGGAGAAGGAGAAAGATGACCAAAAAGTGAGATCTGTCACTGTGTGAA

4920
*

GGACGGATGTGTTAATTGACTTAATTACTAAGTCATCTGTATTAAATTCTGTTATAATGTAAAG

4980
*

AGATTCCAGCCTTGTAAATAATGAATGGAAGACCCTGTGCTGCACTTAAAAGTATTTGCTGCTT

5040
*

GATTATTTCATTTTTACATCAGAGCTTTATAACGAACTTTTGTACAGAATTGTGAGTTGTGACC

Fig. 6E

5100
*

ATGGAACAGTGAGAGGTTTTGCTAGGGCCTATTATTTTTAACCACCATTAATTAGTTGGGGTGG

5160
*

AGTTTACTGTACTGTGAAATTTTCACATTTGAATTTTTTTAATTGCCTGGCAA

Fig. 6F